

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: PARANHOS-BACCALA, Glaucia  
LESENECHAL, Mylene  
JOLIVET, Michel
- (ii) TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, AND  
GENE ENCODING THE LATTER; THEIR APPLICATION TO THE  
DETECTION OF CHAGAS DISEASE
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Oliff & Berridge  
(B) STREET: 700 South Washington Street, Suite 300  
(C) CITY: Alexandria  
(D) STATE: Virginia  
(E) COUNTRY: U.S.A.  
(F) ZIP: 22314
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/480,917  
(B) FILING DATE: 07-JUN-1995  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Berridge, William P.  
(B) REGISTRATION NUMBER: 30,024  
(C) REFERENCE/DOCKET NUMBER: WPB 36400
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 703-836-6400  
(B) TELEFAX: 703-836-2787

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3402 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AACGCTATTA TTAGAACAGT TTCTGTACTA TATTGTCATT TGGGGAGGGG GGAAAGGGGG	60
GAAGTACTTG CCGTTTTGTG TGGGTGACGA GACAACACAC ATCGAGCGGG AAGAAAAAAA	120
AAAAGGAAAT AAATTAAATT AAATTATTG TTCTTTGAAT AGGCAAAGAA GAAGAAGAAG	180

AAAAGGTGCG	GGGGAGGGAG	GAGAAAGCGA	CACACACACA	AAAAAAAAAA	AAGGAATTGC	240
GGAAATAACA	ACGCAAGGCG	CGGACATGAC	CGTGACGGTG	GATTTGTTCA	ATCATGCGAA	300
CCCGAGCAAC	AATGAGGGCC	GCGTGTGGTC	TGTGGACGCC	GCGACATTTA	ACGAGGTGCC	360
TGAGGCGCAG	CGTGTGCTGG	CGGATTTCGA	GTTTATCTT	GCCTACACCA	TGAAGCGGCG	420
TCACGTGCTG	CGTGTGGTGA	AGCGCTCGAA	CCTTTTGAAG	GGCACCCTGC	GGGCACACTC	480
AAAGCCCATT	CATGCGGTGA	AGTTTGTGAA	TTACCGCAGT	AACGTCGCAG	CATCGGCTGG	540
GAAGGGGGAG	TTCTTCGTGT	GGGTTGTGAC	GGATGAAACG	GAGGCGAGCA	ACGGCAAGCC	600
GGATCTCGCA	GCCCGCCTCA	CAGTGAAGGT	GTA CTTTAAG	CTTCAGGATC	CTGTCACAAT	660
TCCATGCTTT	TCTTTCTTTA	TCAACGCCGA	GAGTCAGCGG	CCTGATCTGC	TTGTCCTTTA	720
CGAAACGCAG	GCGGCAATTC	TTGACAGCTC	CTCCCTCATT	GAGCGCTTTG	ACGTGGAATC	780
ACTGGAGGCA	ACACTACAGC	GGAATTGCAC	AACCCTGCGA	ACCCTGACTC	AACCGGTTAG	840
TGAGAACAGT	TTATGCTCCG	TTGGCTCTGG	CGGATGGTTC	ACCTTTACCA	CGGAACCAAC	900
AATGGTAGCG	GCATGCACAT	TACGAAACCG	CAGCACTCCA	TCATGGGCGT	GTTGCGAGGG	960
TGAGCCAGTG	AAGGCATTGC	ATCTCCTTGA	CGCAACCGTT	GAGGAAAATG	TCAGTGTCT	1020
CGTGGCCGCA	TCTACAAAAG	GGGTGTACCA	ATGGCTCCTT	ACGGGTGTAG	CAGAACCAAA	1080
CTTGTTGCGC	AAGTTTGTCA	TTGATGGATC	TATTGTCGCG	ATGGAAAGCT	CACGAGAAAC	1140
GTTTGCCGTG	TTTGACGACA	GGAAGCAGCT	GGCGCTGGTC	AACATGCATT	CCCCTCATAA	1200
CTTTACCTGC	ACACACTACA	TGATGCCTTG	TCAGGTACAG	CGTAACGGCT	TTTGCTTCAA	1260
TCGTACAGCC	GACGGTAGCT	GCGTCCTGGC	TGACATGTCT	ATTCGATTGA	CGATCTTCCA	1320
TCTCCGGTCC	TCCCGCAGGG	AAGAACAGCA	GCCAGGCCAA	AAAACATCGG	TAGTGGCGAC	1380
GGCGAAACCG	GGGTGTGTGT	CCTCGGGCAC	TGAAGCGGCG	AGTAGCAGTC	ATACCAATAC	1440
GA CTTCTGCC	GCTGCTGCAT	CCCCTGCATC	ACCCCTGTT	TCAGCGCCAG	CCAAGGCAGC	1500
CGCGCCTCCT	GCCGCGGCGC	GATCGGCTGA	GCGGCACGTC	GGGAGCAAGA	TCATTGCTAA	1560
TCTAGTGAAT	CAGCTGGGGA	TTAATGTCAC	CCAAAGGAGC	GTCGTCAGCA	CTGGAGCGCC	1620
GGCCACGACG	AGGTCTACGG	CGGTGACGTC	CACGACTACC	GCCCCGCAGC	GAACAAGTCC	1680
ATACGGGCAC	AATGGCCGAC	CTGTGACGGC	TGGATTGGTG	GCAGCTAATA	GTGGTGCCAG	1740
CGCGGCCTCG	TCTCCACAG	CCGCGGCGAA	ACCAACAGGA	GAAGAAAAGG	CCTCCGCGGC	1800
ATGTGAAACG	AGCTCCGTGG	CGATAAATGC	GACACGCCCC	GCGCTTCACA	ACGCCTCTCT	1860
CCCGCAGGCG	CCAACGGATG	GCGTTTTGGC	GGCAGCAGTA	TACCAGTCGG	AGGGCGAGGT	1920
TCATCAGTCG	CTGGAGCGGC	TGGAGTCCGT	CATAACCAAC	ACGTCTCGGG	TTCTGAAGTT	1980
GCTCCCTGAC	ACCATTCGAA	GAGACCATGA	ACA ACTTCTG	AATCTGGGTT	TAGAGGCACA	2040

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GATGACAGAG CTGCAGCAGA GCCGTCCAAC ACCGCAAACA CAGCCGAGAG ACACAAGCTC 2100  
 CGCGAAATCA TCCGTGTTTG AGACGTACAC CCTTGTTCTC ATTGCGGATT CCCTCTCTCG 2160  
 CAACATCACG AAGGGGGTGA AGCGTGGTGT GAACGAGGCC ATTATGTTGC ATCTCGACCA 2220  
 TGAGGTGCGG CACGCCATAG GGAACCGGCT TCGGCAAACA CAAAAGAACA TCATCAAGAG 2280  
 CCGCCTCGAT GAAGCGTTGA AGGAAAGCAC TACACAGTTT ACGGCTCAAT TGACGCAAAC 2340  
 GGTGGAGAAT CTGGTGAAGC GCGAGCTTGC CGAGGTGCTT GGTAGCATCA ACGGCTCCCT 2400  
 CACTTCTCTC GTGAAGGAAA ATGCCTCATT ACAGAAAGAG TTGAATTCCA TAATGTCTAG 2460  
 TGGGGTGTTG GATGAAATGC GTCGTATGCG GGAAGAGCTG TGCACATTGC GAGAGTCCGT 2520  
 TGCGAAGCGG AAGGCAACAA TGCCAGATTC TTCTCTTCAC GCCACGAGCT CCTTTCAAGG 2580  
 AAGAAGGTCT GCGCCCGAGA CAATTCTTGC AACC GCGTTA TCGATGGTGC GAGAGCAGCA 2640  
 ATACCGTCAG GGA CTGGAAT ACATGTTGAT GGCTCAGCAG CCCTCTCTCC TCCTGCGGTT 2700  
 CCTCAGCATA CTTACAAGGG AAAACGAAAA CGCCTACTCG GAACTTATTG AAAATGTAGA 2760  
 GACGCCGAAT GACGTGTGGT GTTCGGTTCT GTTGCAACTC ATAGAGGCCG CGGCGACCGA 2820  
 GGCTGAGAAG GAGGTGGTTG TTGGCGTCGC CATTGATATT CTCTCCGAGC GCGATCAAAT 2880  
 TGCTCAGAAC GGCGCACTCG GCTCGAAACT CACCACCGCC ATGCGAGCCT TTGAGCGACA 2940  
 GGCAAGGTCG GAGACAACGA GCAGGTCATT CTTGCAATGC CTGAAGAACC TGGAAAAGCT 3000  
 TCTGCAATCA TGATAATAAA AAGAACTCAA CGAATACAGT TGTGATTAT TAAGGAAGGG 3060  
 AAAAGAGAGA AAGAGAGAGA GAGAGAGAGA AATGTAATGG GCGTTTAGTT ACGGTAGAAA 3120  
 GAAAACGTGT GGATAAGAAG GAGGGGTTTT GTGTGCGACC AGGAATTACT GGGGAACGCT 3180  
 GCTACACGGC GGAATCGACC ATTTTATTAT TATTATTATT GTCTTTAGTA TTATGTTTTT 3240  
 TCTTGTGTGT GTGTGTGTGT GTTGTGTGT GTGCGGTTAT TTTGTATCCG TTTGCTCCCC 3300  
 CCCCTGCCCC CCATCACCCG AGGAGAAAGT AGAATAAGAC ACATACGATT GTTGTTTTTG 3360  
 TTATCCTTAA AAGGAAGAGA GACCAAAAAA AAAAAAAAAA AA 3402

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Val	Thr	Val	Asp	Leu	Phe	Asn	His	Ala	Lys	Pro	Ser	Asn	Asn	1	5	10	15
Glu	Gly	Arg	Val	Trp	Ser	Val	Asp	Ala	Ala	Thr	Phe	Asn	Glu	Val	Pro	20	25	30	
Glu	Ala	Gln	Arg	Val	Leu	Ala	Asp	Ser	Gln	Phe	Tyr	Leu	Ala	Tyr	Thr	35	40	45	
Met	Lys	Arg	Arg	His	Val	Leu	Arg	Val	Val	Lys	Arg	Ser	Asn	Leu	Leu	50	55	60	
Lys	Gly	Thr	Val	Arg	Ala	His	Ser	Lys	Pro	Ile	His	Ala	Val	Lys	Phe	65	70	75	80
Val	Asn	Tyr	Arg	Ser	Asn	Val	Ala	Ala	Ser	Ala	Gly	Lys	Gly	Glu	Phe	85	90	95	
Phe	Val	Trp	Val	Val	Thr	Asp	Glu	Thr	Asp	Ala	Ser	Asn	Gly	Lys	Pro	100	105	110	
Asp	Leu	Ala	Ala	Arg	Leu	Thr	Val	Lys	Val	Tyr	Phe	Lys	Leu	Gln	Asp	115	120	125	
Pro	Val	Thr	Ile	Pro	Cys	Phe	Ser	Phe	Phe	Ile	Asn	Ala	Glu	Ser	Gln	130	135	140	
Arg	Pro	Asp	Leu	Leu	Val	Leu	Tyr	Glu	Thr	Gln	Ala	Ala	Ile	Leu	Asp	145	150	155	160
Ser	Ser	Ser	Leu	Ile	Glu	Arg	Phe	Asp	Val	Glu	Ser	Leu	Glu	Ala	Thr	165	170	175	
Leu	Gln	Arg	Asn	Cys	Thr	Thr	Leu	Arg	Thr	Leu	Thr	Gln	Pro	Val	Ser	180	185	190	
Glu	Asn	Ser	Leu	Cys	Ser	Val	Gly	Ser	Gly	Gly	Trp	Phe	Thr	Phe	Thr	195	200	205	
Thr	Glu	Pro	Thr	Met	Val	Ala	Ala	Cys	Thr	Leu	Arg	Asn	Arg	Ser	Thr	210	215	220	
Pro	Ser	Trp	Ala	Cys	Cys	Glu	Gly	Glu	Pro	Val	Lys	Ala	Leu	His	Leu	225	230	235	240
Leu	Asp	Ala	Thr	Val	Glu	Glu	Asn	Val	Ser	Val	Leu	Val	Ala	Ala	Ser	245	250	255	
Thr	Lys	Gly	Val	Tyr	Gln	Trp	Leu	Leu	Thr	Gly	Val	Ala	Glu	Pro	Asn	260	265	270	
Leu	Leu	Arg	Lys	Phe	Val	Ile	Asp	Gly	Ser	Ile	Val	Ala	Met	Glu	Ser	275	280	285	
Ser	Arg	Glu	Thr	Phe	Ala	Val	Phe	Asp	Asp	Arg	Lys	Gln	Leu	Ala	Leu	290	295	300	
Val	Asn	Met	His	Ser	Pro	His	Asn	Phe	Thr	Cys	Thr	His	Tyr	Met	Met	305	310	315	320

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Pro	Cys	Gln	Val	Gln	Arg	Asn	Gly	Phe	Cys	Phe	Asn	Arg	Thr	Ala	Asp	325	330	335
Gly	Ser	Cys	Val	Leu	Ala	Asp	Met	Ser	Asn	Arg	Leu	Thr	Ile	Phe	His	340	345	350
Leu	Arg	Cys	Ser	Arg	Arg	Glu	Glu	Gln	Gln	Pro	Gly	Gln	Lys	Thr	Ser	355	360	365
Val	Val	Ala	Thr	Ala	Lys	Pro	Gly	Cys	Val	Ser	Ser	Gly	Thr	Asp	Ala	370	375	380
Ala	Ser	Ser	Ser	His	Thr	Asn	Thr	Thr	Ser	Ala	Ala	Ala	Ala	Ser	Pro	385	390	395
Ala	Ser	Pro	Pro	Val	Ser	Ala	Pro	Ala	Lys	Ala	Ala	Ala	Pro	Pro	Ala	405	410	415
Ala	Ala	Arg	Ser	Ala	Glu	Pro	His	Val	Gly	Ser	Lys	Ile	Ile	Ala	Asn	420	425	430
Leu	Val	Asn	Gln	Leu	Gly	Ile	Asn	Val	Thr	Gln	Arg	Ser	Val	Val	Ser	435	440	445
Thr	Gly	Ala	Pro	Ala	Thr	Thr	Arg	Ser	Thr	Ala	Val	Thr	Ser	Thr	Thr	450	455	460
Thr	Ala	Pro	Gln	Arg	Thr	Ser	Pro	Tyr	Gly	His	Asn	Gly	Arg	Pro	Val	465	470	475
Thr	Ala	Gly	Leu	Val	Ala	Ala	Asn	Ser	Gly	Ala	Ser	Ala	Ala	Ser	Ser	485	490	495
Pro	Thr	Ala	Ala	Ala	Lys	Pro	Thr	Gly	Glu	Glu	Lys	Ala	Ser	Ala	Ala	500	505	510
Cys	Glu	Thr	Ser	Ser	Val	Ala	Ile	Asn	Ala	Thr	Arg	Pro	Ala	Leu	His	515	520	525
Asn	Ala	Ser	Leu	Pro	Gln	Ala	Pro	Thr	Asp	Gly	Val	Leu	Ala	Ala	Ala	530	535	540
Val	Tyr	Gln	Ser	Glu	Gly	Glu	Val	His	Gln	Ser	Leu	Glu	Arg	Leu	Glu	545	550	555
Ser	Val	Ile	Thr	Asn	Thr	Ser	Arg	Val	Leu	Lys	Leu	Leu	Pro	Asp	Thr	565	570	575
Ile	Arg	Arg	Asp	His	Glu	Gln	Leu	Leu	Asn	Leu	Gly	Leu	Glu	Ala	Gln	580	585	590
Met	Thr	Glu	Leu	Gln	Gln	Ser	Arg	Pro	Thr	Pro	Gln	Thr	Gln	Pro	Arg	595	600	605
Asp	Thr	Ser	Ser	Ala	Lys	Ser	Ser	Val	Phe	Glu	Thr	Tyr	Thr	Leu	Val	610	615	620
Leu	Ile	Ala	Asp	Ser	Leu	Ser	Arg	Asn	Ile	Thr	Lys	Gly	Val	Lys	Arg	625	630	635
Gly	Val	Asn	Glu	Ala	Ile	Met	Leu	His	Leu	Asp	His	Glu	Val	Arg	His	645	650	655

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Ala Ile Gly Asn Arg Leu Arg Gln Thr Gln Lys Asn Ile Ile Lys Ser  
660 665 670

Arg Leu Asp Glu Ala Leu Lys Glu Ser Thr Thr Gln Phe Thr Ala Gln  
675 680 685

Leu Thr Gln Thr Val Glu Asn Leu Val Lys Arg Glu Leu Ala Glu Val  
690 695 700

Leu Gly Ser Ile Asn Gly Ser Leu Thr Ser Leu Val Lys Glu Asn Ala  
705 710 715 720

Ser Leu Lys Lys Glu Leu Asn Ser Ile Met Ser Ser Gly Val Leu Asp  
725 730 735

Glu Met Arg Arg Met Arg Glu Glu Leu Cys Thr Leu Arg Glu Ser Val  
740 745 750

Ala Lys Arg Lys Ala Thr Met Pro Asp Ser Ser Leu His Ala Thr Ser  
755 760 765

Ser Phe Gln Gly Arg Arg Ser Ala Pro Glu Thr Ile Leu Ala Thr Ala  
770 775 780

Leu Ser Met Val Arg Glu Gln Gln Tyr Arg Gln Gly Leu Glu Val Met  
785 790 795 800

Leu Met Ala Gln Gln Pro Ser Leu Leu Leu Arg Phe Leu Ser Ile Leu  
805 810 815

Thr Arg Glu Asn Glu Asn Ala Tyr Ser Glu Leu Ile Glu Asn Val Glu  
820 825 830

Thr Pro Asn Asp Val Trp Cys Ser Val Leu Leu Gln Leu Ile Glu Ala  
835 840 845

Ala Ala Thr Glu Ala Glu Lys Glu Val Val Val Gly Val Ala Ile Asp  
850 855 860

Ile Leu Ser Glu Arg Asp Gln Ile Ala Gln Asn Gly Ala Leu Gly Ser  
865 870 875 880

Lys Leu Thr Thr Ala Met Arg Ala Phe Glu Arg Gln Ala Arg Ser Glu  
885 890 895

Thr Thr Ser Arg Ser Phe Leu Gln Cys Leu Lys Asn Leu Ile Lys Leu  
900 905 910

Leu Gln Ser  
915

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phage DNA"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "phage DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGACACCAG ACCAACTGGT AATG

24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCGGGCACTG ACGCGGCG

18

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "phage lambda gt10 DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTATGAGTA TTTCTTCCAG GGTA

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACGCTATTA TTAGAACAGT T

21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCAGCAGCG GCAGAAGT

18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCCGACGG TAGCTGCGTC CT

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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1864280 SE28E16



ACATAATGGC CTCGTTGACA C

21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GACTCGCTGC AGATCGATTT TTTTTTTTTT TTTT

34

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAAGAGACC ATGAACAACT T

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACTCGCTGC AGATCGAT

18

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864280-5E78E760